Amendments to the Claims:

There are no amendments to the claims. This listing of claims is for the convenience of the Examiner and replaces all prior versions, and listings of claims in the application:

Listing of Claims:

Claims 1-38. (canceled)

Claim 39. (previously presented) A method for identification of a nucleic acid molecule that modulates a process in a biological system comprising the steps of:

a) introducing a random library of a nucleic acid catalyst into said biological system under conditions suitable for modulating said process, wherein said nucleic acid catalyst comprises a substrate binding domain and a catalytic domain, said substrate binding domain comprises a random sequence; and

b) determining the nucleotide sequence of at least a portion of the substrate binding domain of said nucleic acid catalyst from said biological system in which the process has been modulated.

Claim 40. (previously presented) A method for identifying one or more nucleic acid molecules involved in a process in a biological system comprising the steps of:

a) providing a library of a nucleic acid catalyst, with a substrate binding domain and a catalytic domain, wherein said substrate binding domain comprises a random sequence, to said biological system under conditions suitable for said process to be altered;

b) identifying any said nucleic acid catalyst present in said biological system where said process has been altered; and

c) determining the nucleotide sequence of at least a portion of the binding domain of said any said nucleic acid catalyst to allow said identification of said nucleic acid molecule involved in said process in said biological system.

Claim 41. (previously presented) A method for identification of a nucleic acid catalyst that modulates a process in a biological system comprising the steps of:

a) introducing a random library of a nucleic acid catalyst into said biological system under conditions suitable for modulating said process, wherein said nucleic acid catalyst comprises a substrate binding domain and a catalytic domain, said substrate binding domain comprises a random sequence; and

b) identifying said nucleic acid catalyst from said biological system in which the process has been modulated.

Claim 42. (previously presented) The method of any of claims 39-41, wherein said biological system is a bacterial cell.

Claim 43. (previously presented) The method of any of claims 39-41, wherein said biological system is of plant origin.

Claim 44. (previously presented) The method of any of claims 39-41, wherein said biological system is of mammalian origin.

Claim 45. (previously presented) The method of any of claims 39-41, wherein said nucleic acid catalyst is in a hammerhead motif.

Claim 46. (previously presented) The method of any of claims 39-41, wherein said nucleic acid catalyst is in a hairpin motif.

Claim 47. (previously presented) The method of any of claims 39-41, wherein said nucleic acid catalyst is in a group I intron ribozyme motif, group II intron ribozyme motif, VS ribozyme motif or RNase P ribozyme motif.

Claim 48. (previously presented) The method of any of claims 39-41, wherein said process is selected from the group consisting of growth, proliferation, apoptosis, morphology, angiogenesis, differentiation, migration, viral multiplication, drug resistance, signal transduction, cell cycle regulation, temperature sensitivity and chemical sensitivity.

Claim 49. (previously presented) The method of any of claims 39-41, wherein said random library of nucleic acid catalysts is encoded by an expression vector in a manner which allows expression of said nucleic acid catalysts.

Claim 50. (previously presented) The method of claim 49, wherein said expression vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) a sequence encoding at least one said nucleic acid catalyst; and

wherein said sequence is operably linked to said initiation region and said termination region, in a manner which allows expression or delivery or expression and delivery of said nucleic acid catalyst.

Claim 51. (previously presented) The method of claim 49, wherein said expression vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) an open reading frame for a polypeptide;

d) a sequence encoding at least one said nucleic acid catalyst,

wherein said sequence is operably linked to the 3'-end of said open reading frame; and

wherein said sequence is operably linked to said initiation region, said open reading frame and said termination region, in a manner which allows expression or delivery or expression and delivery of said nucleic acid catalyst.

Claim 52. (previously presented) The method of claim 49, wherein said expression vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) an intron;

d) a sequence encoding at least one said nucleic acid catalyst; and

wherein said sequence is operably linked to said initiation region, said intron and said termination region, in a manner which allows expression or delivery or expression and delivery of said nucleic acid catalyst.

Claim 53. (previously presented) The method of claim 49, wherein said expression vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) an intron;

d) an open reading frame for a polypeptide;

e) a sequence encoding at least one said nucleic acid catalyst,

wherein said sequence is operably linked to the 3'-end of said open reading frame; and

wherein said sequence is operably linked to said initiation region, said intron, said open reading frame and said termination region, in a manner which allows expression or delivery or expression and delivery of said nucleic acid catalyst.

Claim 54. (previously presented) The method of claim 49, wherein said expression vector is derived from a retrovirus.

Claim 55 . (previously presented) The method of claim 49, wherein said expression vector is derived from an adenovirus.

Claim 56. (previously presented) The method of claim 49, wherein said expression vector is derived from an adeno-associated virus.

Claim 57. (previously presented) The method of claim 49, wherein said expression vector is derived from an alphavirus.

Claim 58. (previously presented) The method of claim 49, wherein said expression vector is derived from a bacterial plasmid.

Claim 59. (previously presented) The method of claim 49, wherein said expression vector is operably linked to a RNA polymerase II promoter element.

Claim 60. (previously presented) The method of claim 49, wherein said expression vector is operably linked to a RNA polymerase III promoter element.

Claim 61. (previously presented) The method of claim 49, wherein said RNA polymerase III promoter is derived from a transfer RNA gene.

Claim 62. (previously presented) The method of any of claims 39-41, wherein said biological system is of an eukaryotic origin.

Claim 63. (previously presented) The method of any of claims 39-41, wherein said biological system is of a prokaryotic origin.

Claim 64. (previously presented) The method of any of claims 39-41, wherein said substrate binding domain is of length between 12 and 100 nucleotides.

Claim 65. (previously presented) The method of any of claims 39-41, wherein said substrate binding domain is of length between 14 and 24 nucleotides.

Claim 66. (previously presented) The method of any of claims 39-41, wherein said nucleic acid catalyst comprises two substrate binding arms.

Claim 67. (previously presented) The method of claim 66, wherein said substrate binding arms are of similar length.

Claim 68. (previously presented) The method of claim 66, wherein said substrate binding arms are of different length.

Claim 69. (previously presented): A method for identifying a gene that modulates a process in a biological system comprising the steps of:

a) introducing a library of nucleic acid catalysts into a biological system under conditions suitable for modulating a process in the biological system, wherein each nucleic acid catalyst comprises a substrate binding domain and a catalytic domain and the substrate binding domain comprises a random sequence;

b) determining the nucleotide sequence of at least a portion of the substrate binding domain of any nucleic acid catalyst in the biological system in which the process has been modulated; and

c) identifying a gene that modulates a process in a biological system using the nucleotide sequence from step (b).

Claim 70. (previously presented): A method for identifying a gene involved in a biological process comprising the steps of:

a) introducing a library of nucleic acid catalysts into a biological system under conditions suitable for altering a process in the biological system, wherein each nucleic acid catalyst comprises a substrate binding domain and a catalytic domain and the substrate binding domain comprises a random sequence;

b) identifying any nucleic acid catalyst in the biological system in which the biological process has been altered; and

c) determining the nucleotide sequence of at least a portion of the substrate binding domain of any nucleic acid catalyst from step (b) to identify a gene involved in said biological process.

Claim 71. (previously presented): A method comprising the steps of:

a) providing a random binding arm nucleic acid catalyst library to a biological system under conditions suitable for a nucleic acid catalyst from the library to down-regulate the expression of a gene;

b) determining the biological system in which the expression of a gene has been down-regulated;

c) determining the nucleotide sequence of at least one portion of the binding arm of the nucleic acid catalyst in the biological system of step (b); and

d) identifying the gene which expression is down-regulated using the nucleotide sequence from step (c).

Claim 72. (previously presented): The method of any of claims 69-71, wherein said nucleic acid catalyst is in a group I intron ribozyme motif, group II intron ribozyme motif hepatitis delta virus ribozyme motif, VS ribozyme motif or RNase P ribozyme motif.

Claim 73. (previously presented): The method of any of claims 69-71, wherein said nucleic acid catalyst is in a hammerhead ribozyme motif.

Claim 74. (previously presented): The method of any of claims 69-71, wherein said nucleic acid catalyst is in a hairpin ribozyme motif.

Claim 75. (previously presented): The method of any of claims 69-71, wherein said biological system is a bacterial cell.

Claim 76. (previously presented): The method of any of claims 69-71, wherein said biological system is of plant origin.

Claim 77. (previously presented): The method of any of claims 69-71, wherein said biological system is of mammalian origin.

Claim 78. (previously presented): The method of claim 69 or claim 70, wherein said process is selected from the group consisting of growth, proliferation, apoptosis, morphology, angiogenesis, differentiation, migration, viral multiplication, drug resistance, signal transduction, cell cycle regulation, temperature sensitivity and chemical sensitivity.

Claim 79. (previously presented): The method of any of claims 69-71, wherein said library of nucleic acid catalysts is encoded by an expression vector in a manner which allows expression of said nucleic acid catalysts.

Claim 80. (previously presented): The method of claim 79, wherein said expression vector comprises:

a) a transcription initiation region;

b) a transcription termination region; and

c) a sequence encoding at least one said nucleic acid catalyst,

wherein said sequence is operably linked to said initiation region and said termination region, in a manner which allows expression or delivery or expression and delivery of said nucleic acid catalyst.

Claim 81. (previously presented): The method of claim 79, wherein said expression vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) an open reading frame for a polypeptide; and

d) a sequence encoding at least one said nucleic acid catalyst,

wherein said sequence is operably linked to the 3'-end of said open reading frame; wherein said sequence is operably linked to said initiation region, said open reading frame and said termination region, in a manner which allows expression or delivery or expression and delivery of said nucleic acid catalyst.

Claim 82. (previously presented): The method of claim 79, wherein said expression vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) an intron; and

d) a sequence encoding at least one said nucleic acid catalyst,

wherein said sequence is operably linked to said initiation region, said intron and said termination region, in a manner which allows expression or delivery or expression and delivery of said nucleic acid catalyst.

Claim 83. (previously presented): The method of claim 79, wherein said expression vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) an intron;

d) an open reading frame for a polypeptide; and

e) a sequence encoding at least one said nucleic acid catalyst,

wherein said sequence is operably linked to the 3'-end of said open reading frame; wherein said sequence is operably linked to said initiation region, said intron, said open reading frame and said termination region, in a manner which allows expression or delivery or expression and delivery of said nucleic acid catalyst.

Claim 84. (previously presented): The method of claim 79, wherein said expression vector is derived from a retrovirus.

Claim 85. (previously presented): The method of claim 79, wherein said expression vector is derived from an adenovirus.

Claim 86. (previously presented): The method of claim 79, wherein said expression vector is derived from an adeno-associated virus.

Claim 87. (previously presented): The method of claim 79, wherein said expression vector is derived from an alphavirus.

Claim 88. (previously presented): The method of claim 79, wherein said expression vector is derived from a bacterial plasmid.

Claim 89. (previously presented): The method of claim 79, wherein said expression vector is operably linked to a RNA polymerase II promoter element.

Claim 90. (previously presented): The method of claim 79, wherein said expression vector is operably linked to a RNA polymerase III promoter element.

Claim 91. (previously presented): The method of claim 90, wherein said RNA polymerase III promoter is derived from a transfer RNA gene.

Claim 92. (previously presented): The method of any of claims 69-71, wherein said biological system is of an eukaryotic origin.

Claim 93. (previously presented): The method of any of claims 69-71, wherein said biological system is of an prokaryotic origin.

Claim 94. (previously presented): The method of any of claims 69-71, wherein said substrate binding domain is of a length between 12 and 100 nucleotides.

Claim 95. (previously presented): The method any of claims 69-71, wherein said substrate binding domain is of a length between 14 and 24 nucleotides.

Claim 96. (previously presented): The method of any of claims 69-71, wherein said substrate binding domain comprises two substrate binding arms.

Claim 97. (previously presented): The method of claim 96, wherein said substrate binding arms are of similar length.

Claim 98. (previously presented): The method of claim 96, wherein said substrate binding arms are of different length.